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GAAGGAGATCCAAAAGCTTGAAACGGAGTTACAAGAGGCTACCAAAGAATTCCAGATTAAAGAGG
ATATTCCTGAAACAAAGATGAAATTCTTATCAGTTGAAACTCCTGAGAATGACAGCCAGTTGTCA
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TATCACCTTTGAAAAAGAAGAAGTTGCTCAAAATGTGGTAAGCATGAGTAAACATCATGTACAGA
TAAAAGATGTAAATCTGGAGGTTACGGCCAAGCCAGTTCCATTAAATTCAGGAGTCAGATTCCAG
GTTTATGTAGAAGTTTCTAAAATGAAAATCAATGTTACTGAAATTCCTGACACATTGCGTGAAGA
TCAAATGAGAGACAACTAGAGCTGAGCTTTTCAAAGTCCCGAAATGGGAGGCGGAGANGTGGAC
CGCGTGGGACTATGACAGACAGTCCGGGAGTGCAATCATCACGTTTGGNGGAGATTGGGAGTGGC
TGACANN (SEQ ID NO: 4)

Figure 1

Hou c6/#1

CGGAGTTACAAGAGGCTACCAAAGAATTCCAGATTAAAGAGGATATTCCTGAAACAAAGATGAAA
TTCTTATCAGTTGAAACTCCTGANAATGACAGCCAGTTGTCAAATATCTCCTGTTTCGTTTCAAGG
TGAGCTCGAAAGTTCCTTATGAGATACAAAAAGGACAATGCACTTATCACCTTTGAAAAAGGAAG
AAGTTGCTCAAAATGTGNGTAANGCATGAGTAAACATCATGTACAGATAATAAGATGTAAATCTG
GAGGTTACGGCCAAAGCCAAGTTCCATTAATATTCAAGGAGTCANGATTCCAGNGTTTATGCTAG
AANGTTTCTAAAAATGANAATCAATGGTTACTGGAAATTCCTGGACACATTGCGNTGAAAGATCA
AGATGACGAAGACAACTAAGAAGCTGAGCTTTTCAAAAGTCCCGAAANATGGAAGAGCGGTAGA
GGGTGGNACCGCGTGNGANCTATGACAAGACAAGNCCGGGGGAAGNTGCAGTCCATCACGTTTGTN
NGAAGATTGGANGTNGGCTGACCAANGAATTTTGAAAAAGGAGANGAATTACCCCTCTTTANGAG
TAANATCAAAACCCTGCCATAANAAGTTNACTGGTTTCNCCCATTACACAGNAN
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CTTCTGGACAANGGT (SEQ ID NO: 5)

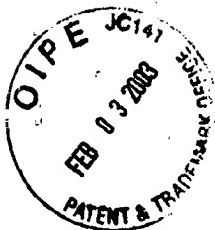
Figure 2

Hou c17/#2

c6/#1	1	HEGRGI	DKDDTQQILKEHSPDEFIKDEQNKGL	ITKKNIQLKKEIQKLETELQEA
Hou/Nmi	1	-----	DKDDTQQILKEHSPDEFIKDEQNKGL	ITKKNIQLKKEIQKLETELQEA
c6/#1	61	TKEFQIKEDIPETKMKFLSVETPENDS	QLSNISCSFQVSSKVPYEQKGQALITFEKEEV	
Hou/Nmi	55	TKEFQIKEDIPETKMKFLSVETPENDS	QLSNISCSFQVSSKVPYEQKGQALITFEKEEV	
c6/#1	121	AQNVVSMKHHVQIKDVNLEVTA	KPVPLNSGVRFQVYVEVSKMKINVTEIPDTLREDQMR	
Hou/Nmi	115	AQNVVSMKHHVQIKDVNLEVTA	KPVPLNSGVRFQVYVEVSKMKINVTEIPDTLREDQMR	
c6/#1	181	DKLELSFSKSRNGRRRCGPR	GTMTDSPGVQSSRLVEIGS	-----
Hou/Nmi	175	DKLELSFSKFRNGGGEV.DR	VVDYDRQSGSAVITFVEIGV	DKILKKKEYPLYINQCHRV
c6/#1	221	-----	-----	-----
Hou/Nmi	234	TVSPYTEIHLKKYQIFSGTSKRTVLLTGMEGIQMDREIVEDLINIH	FQRAKNGGGEVDVV	
c6/#1	221	-----	(SEQ 10 NO:6)	
Hou/Nmi	294	KCSLGQPHIAYFEE	(SEQ 10 NO:7)	

Figure 3

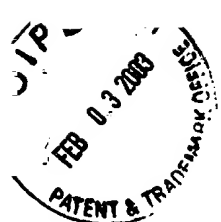




AGCAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGCAGGTC
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TCTTCTTTGGCAAGACTAGGAACGGAGGTGGCNATGTGGACNTTCGGGANCTACTGCCAGGGANT
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GGCTTTNTG(SEQ ID NO. 8)

Figure 4

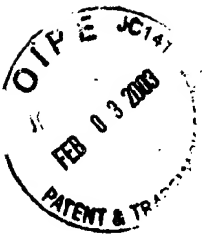
IFP35 c14/#1



CCAAAGTGGCTGAGCAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGC
AGGTCCAGCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGTCCAGCCAGTTGAGTGGCCGGAGGGTGT
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GCAAGACTAGGAACGGAGGTGGCGATGTGGACGTTCTGGGAGCTACTGCCAGGGAGTGTGATGCTGGGGTTTG
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CCTCTGAGAGTCTCTCCGTATGTGAATGGGGAGATCCAGAAGGCTGAGATCAGGTCGCANCCAGTTCCCCNC
TCGGTACTGGGTGCTCAACATTCTGATATCTTGGATTGGCCCCGGAGCTGCATNACGTCTGGANATCAACT
TCANAAGCCCACCCGCCGGGGCNGNGAGGTANAAGGCCTGACATCNTTACCCCAAAGGACAGCATGGNCCTA
ACAGTCCTCACCTCCNAATCANGCTNNGGGGCTNCCCTTCTANCNTCCCCAACTG (SEQ ID NO: 9)

Figure 5

IFP35 c33/#2



GGATCCACTGCCCTCTGCTTGCGGGCTCTGCTCTGATCACCTTTGATGACCCCAAAGTGGCTGAG
CAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGCAGGTCCA
GCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGATGGTGTCCAGCCANTTGAGTGGCCGGA
GGGTGTTGGTCACTGGATTTCTGCCAGCCTCAGGCTGANTGAGGAGGAGCTGCTGGACAAGCTA
TGAGATCTTCTTTGGCAANACTANGAACGGANGTGGCGATGTGGACGTTCTGGGAGCTACTGCCAG
GGAGTGTCATGCTGGGGTTTGCTACGGATGGAGTGGCTCAGCGTCTGTGCCAAATCGGCCAGTTC
ACAAGTGCCACTGGGTGGGCAGCAAGTCCCTCTGAGAGTCTCTCCGTATGTGANTGGNGAGATCA
GAATGCTGANATTAAGTCGCATCCAATTCCTCGCTCNGGTACTGGTGCTCANNATCCTGANATCT
TGGATTGGCCCCNGANTNCATGANATCTGGNAGATTCAATTNCANAAGTCCANCCNNCNGNGNCG
GGAAGTANANGCCCGANANTTCNTNNCNTANGGNCAGCANNGCCTG (Seq 10 NO: 10)

Figure 6

IFP35 c51/#3

331fn	1	-----
In35_Human	1	MSAPLDAALHALQEEQARLKMLWDLQQLRKELGDSPKDKVPFSPVKIPLVFRGHTQQDP
C51	1	-----
331fn	1	-----HRCPKVAEQVLQOKEHTINMEECRLRVQVQPLELPM
In35_Human	61	EVPKSLVSNLRIHCPLLAGSALITFDDPKVAEQVLQOKEHTINMEECRLRVQVQPLELPM
C51	1	-----HEGRIHCPLLAGSALITFDDPKVAEQVLQOKEHTINMEECRLRVQVQPLELPM
331fn	37	VTTIQ..VSSQLSGRRVLVTGFPA SLRLSEEELLDKLEIFFCKTRNGGGD VDVRELLPGS
In35_Human	121	VTTIQ..VSSQLSGRRVLVTGFPA SLRLSEEELLDKLEIFFCKTRNGGGD VDVRELLPGS
C51	54	VTTIQVMVSSXLSGRRVLVTGFPA SLRLXEEELLDKL*DLLWQXXERXWRC.....
331fn	95	VMLGFARDGVAQRLCQIGQVHSATGWASSPSESLSVCEWGDPE-----
In35_Human	179	VMLGFARDGVAQRLCQIGQFTVPLGGQQVPLRVSPYVNGEIQKAEIRSQPVPRSVLVLNI
C51	104GRSGATARECHAGVCYGWSGSASVPMRPFVHKCHWVGSKSL*ESLRM*XRSEC*X
331fn	139	----- (SEQ ID NO: 11)
In35_Human	239	PDILDGPELHDVLEIHFOXPTRGGGGRCPDSRTPRTAGPSSLHL----- (SEQ ID NO: 12)
C51	156	*VASNSSLXYWCSXS*XLGLAPXXMXSGRFNXXSPXXXXGKXXPXXSXXXXXSXA (SEQ ID NO: 13)

Figure 7



Abp2	1	RLRNGHVGISFVPKETGEHLVHVKNNGQHVASSPIPVVISQSEIGDASRVVRVSGQGLHEG
C50	1	-----
C57	1	-----
Abp2	61	HTFEPAEFIIDTRDAGYGGLSLSIEGFSKVDINTEDLEDGTCRVTYC PTEPGNYIINIKE
C50	1	-----
C57	1	-----HEGR PTEPGNYIINIKE
Abp2	121	ADQHVPGPSFVSVKVTGEGRVKESITRRRRAPSVANVGSHCDLSLKIPEISIQDNTAQVTS
C50	1	-----
C57	18	ADQHVPGPSFVSVKVTGEGRVKESITRRRRAPSVANVGSHCDLSLKIPEISIQDNTAQVTS
Abp2	181	PSGKTHEAEIVEGENHTYCI RFVPAEMGTHTVSVKYKGQHVPGPSPFQFTVGPLGEGGAHK
C50	1	-----
C57	78	PSGKTHEAEIVEGENHTYCI RFVPAEMGTHTVSVKYKGQHVPGPSPFQFTVGPLGEGGAHX
Abp2	241	VRAGGPGLEKAEKGVPAEFS. IWTREAGAGGLAXAVEGPKAEISFEDRKDGSCGVAYVV
C50	1	-----
C57	138	VRAGGPGLEKES* SWSASRIQYLGPGLVLEKWPILSXAPLXLISLLRTARTAPVLLMEV
Abp2	300	QEPGDYEVSVKFNEEHIPDSPFVVPVASPSGDARRLTVSSLQESGLKVNQPASFAVSLNG
C50	1	-----
C57	197	KEPSD* XNPXQVSTKEHX -----
Abp2	360	AKGAIDAKVHSPSGALEECYVTEIDQDKYAVRFIPRENGVYLIDVKFNGTHIPGSPFKIR
C50	1	-----
C57	214	-----
Abp2	420	VGEFGHGDPGLVSAYGAGLEG. GVTGNPAEFVVNTSNAGAGALSVTIDGPSKVKMDCQE
C50	1	-----HEGR GVTGNPAEFVVNTSNAGAGALSVTIDGPSKVKMDCQE
C57	214	-----
Abp2	479	CPEGYRVTYTPMAPGSYLISIKYGGPYHIGGSPFKAKVTGPRLVSNHSLHETSSVFVDSL
C50	42	CPEGYRVTYTPMAPGSYLISIKYGGPYHIGGSPFKAKVTGPRLVSNHSLHETSSVFVDSL
C57	214	-----
Abp2	539	TKATCAPQH GAGPGPADASKVVAKGLGLSKAYVGO KSSFTVDCSKAGNNMLLVGVHGP
C50	102	TKATCAPH H GAGPGPADASKVVAKGLGLSKAYVCH KSSFTVDCSKACIIMLLVGVHGPW
C57	214	-----
Abp2	599	TPC EILVKHVGS. RLYSVSYLLKDKGE. YTLVVKWGHEHIPGSPYRVVVP- (SEQ ID NO: 14)
C50	162	TPC EILVKARGQPALQRVLTCPKDKGEVHTGGQNGGDYQIPCKPLPFCGCP (SEQ ID NO: 15)
C57	214	----- (SEQ ID NO: 16)

Figure 8

